

RAW SEQUENCE LISTING PATENT APPLICATION US/08/815,773

DATE: 04/30/97 TIME: 14:54:29

INPUT SET: S17329.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

1 2		SEQUENCE LISTING FALS
3 4	(1) G	SEQUENCE LISTING ENTER
5 6 7 8 9	(i)	APPLICANT: Baumgartner, James W. Farrah, Theresa M. Foster, Donald C. Grant, Frank J. O'Hara, Patrick J.
11 12	(ii)	TITLE OF INVENTION: Testis-Specific Receptor
13 14	(iii)	NUMBER OF SEQUENCES: 33
15 16 17 18 19 20 21 22	(iv)	CORRESPONDENCE ADDRESS: (A) ADDRESSEE: ZymoGenetics, Inc. (B) STREET: 1201 Eastlake Avenue East (C) CITY: Seattle (D) STATE: WA (E) COUNTRY: USA (F) ZIP: 98102
23 24 25 26 27 28	(V)	COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
29 30 31 32 33	(vi)	CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: (B) FILING DATE: (C) CLASSIFICATION:
34 35 36 37 38	(viii)	ATTORNEY/AGENT INFORMATION: (A) NAME: Parker, Gary E. (B) REGISTRATION NUMBER: 31,648 (C) REFERENCE/DOCKET NUMBER: 95-33
39 40 41 42 43	(ix)	TELECOMMUNICATION INFORMATION: (A) TELEPHONE: 206-442-6673 (B) TELEFAX: 206-442-6678
44 45	(2) INFO	RMATION FOR SEQ ID NO:1:
46	(i)	SEQUENCE CHARACTERISTICS:

RAW SEQUENCE LISTING PATENT APPLICATION US/08/815,773

INPIIT SET: S17329 mw

DATE: 04/30/97 TIME: 14:54:33

(A) LENOTH: 1289 base pairs (B) TYPE: nucleic acid (9) (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (A) SEQUENCE DESCRIPTION: SEQ ID NO:1: (CCCCCCCCCCC GGGAGAGAGG CAATATCAAG GTTTTAAATC TCGGAGAA ATG GCT TTC (A) CCCCCCCCCC GGGAGAGAGG CAATATCAAG GTTTTAAATC TCGGAGAA ATG GCT TTC (B) CCCCCCCCCC GGGAGAGAGG CAATATCAAG GTTTTAAATC TCGGAGAA ATG GCT TTC (B) CTT TGC TTG GCT ATC GGA TGC TTA TAT ACC TTT CTG ATA AGC ACA ACA (IOS (A) CYAL CYAL ELU ALA ILE GLY CYS LEU TYT Thr Phe Leu ILE Ser Thr Thr (B) CTT TGC TTG GCT ATC TGA GAC ACC GAG ATA AAA GTT AAC CCT CCT (B) CTT GGC TGT ACT TCA TCT TCA GAC ACC GAG ATA AAA GTT AAC CCT CCT (B) CTT GGC TGT ACT TCA TCT TCA GAC ACC GAG ATA AAA GTT AAC CCT CCT (CCCCCCCCCC CCC CCC CCC CCC CCC CCC CCC															II!	VPUT	SET: SI	17329.raw
(C) STRANDENNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: CDNA (ix) FEATURE: (A) NAME/KEY: CDS (A) NAME/KEY: CDS (B) LOCATION: 491191 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: (CCCCCCGCCC GGGAGAGAGG CAATATCAAG GTTTTAAATC TCGGAGAA ATG GCT TTC Met Ala Phe 1 (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: (GTT TGC TTG GCT ATC GGA TGC TTA TAT ACC TTT CTG ATA AGC ACA ACA 105 (Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile Ser Thr Thr 168 (TTT GC TGT ACT TCA TCT TCA GAC ACC GAG ATA AAA GTT AAC CCT CCT 153 (A) CAG GAT TTT GAG ATA GTG GAT CCC GGA TAC TTA GGT TAT CTC TAT TTG 201 (CAG GAT TTT GAG ATA GTG GAT CCC GGA TAC TTA AGT TCT TTT TGC ATA AGC ACA GTG 40 Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu Gln Try Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu Cys Thr Val 65 (CAA TGG CAA CCC CCA CTG TCT CTG GAT CAT TTT AAG GAA TGC ACA GTG 249 GIn Try Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu Cys Thr Val 65 (GLu Tyr Glu Leu Lys Tyr Arg Ash Ile Gly Ser Glu Thr Try Lys Thr 70 (GL TAT ACT AAG AAT CTA CAT TAC AAA GAT GGG TTT GAT CTT TA CA AAG ACC 297 GIN TYR Glu Leu Lys Tyr Arg Ash Ile Gly Ser Glu Thr Try Lys Thr 70 (GC ATT GAA GCG AAG ATC CAC ACA TTA CAC AT TAC CAC TTT AAC AAG 345 (Ile Ile Thr Lys Ash Leu His Tyr Lys Asp Gly Phe Asp Leu Ash Lys 16 (GC ATT GAA GCG AAG ATT CAC ACA CCT TTT CCTG GAT ACT TTT CCT TTT TAC CAC ACT CTT AAC AAG 345 (Ile Ile Thr Lys Ash Leu His Tyr Lys Asp Gly Phe Asp Leu Ash Lys Ile His Thr Leu Leu Pro Try Gln Cys Thr Ash 193 (Ile Ile Thr Lys Ash Cac Aca CCT TTA CAC AGG TTT TT TTA TGG AAT ACC ACT ATT TAC AAA ACT TAC AAA GCT TAT TTA CTA TAC AAA ATT TAC AAT TAC AATT TAC AA	47			(2	A) L	ENGTI	H: 13	289	base	pai	rs							
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57 (B) LOCATION: 491191 58 59 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: 61 62 CCCCCGCCC GGGAGAGAGG CAATATCAAG GTTTTAAATC TCGGAGAA ATG GCT TTC 63 Met Ala Phe 64 1 65 66 GTT TGC TTG GCT ATC GGA TGC TTA TAT ACC TTT CTG ATA AGC ACA ACA 67 Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile Ser Thr Thr 68 5 10 69 70 TTT GGC TGT ACT TCA TCT TCA GAC ACC GAG ATA AAA GTT AAC CCT CCT 71 Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val Asn Pro Pro 72 20 25 30 35 73 74 CAG GAT TTT GAG ATA GTG GAT CCC GGA TAC TTA GGT TAT CTC TAT TTG 75 Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu 76 40 45 50 77 78 CAA TGG CAA CCC CCA CTG TCT CTG GAT CAT TTT AAG GAA TGC ACA GTG 79 Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu Cys Thr Val 76 55 60 77 80 GAA TAT GAA CTA AAA TAC CGA AAC ATT GGT AGT GAA ACA TGG AAG ACC 81 Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr Trp Lys Thr 84 70 75 80 85 86 ATC ATT ACT AAG AAT CTA CAT TAC AAA GAT GGG TTT GAT CTT AAC AAG 79 GGA TCA GAA GGC AAG ATA CAC ACG CTT TTA CCA TGG CAA TGC ACA AAT 79 GLY THE CAT TAC AAG AAT CTA CAT TAC AAA GAT GGG TTT GAT CTT AAC AAG 85 90 86 ATC ATT GAA GCG AAG ATA CAC ACG CTT TTA CCA TGG CAA TGC ACA AAT 87 Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys 86 85 90 97 96 98 GGC ATT GAA GGT CAA AGT TCC TGG GAA ACT ACT TAT TGG ATA TCA 99 GGA TCA GAA GTT CAA AGT TCC TGG GCA GAA ACT ACT TAT TGG ATA TCA 441 99 GGA TCA GAA GTT CAA AGT TCC TGG GCA GAA ACT ACT TAT TGG ATA TCA 441 99 GGA TCA GAA GTT CAA AGT TCC TGG GCA GAA ACT ACT TAT TGG ATA TCA 99 GGA TCA GAA GTT CAA AGT TCC TGG GCA GAA ACT ACT TAT TGG ATA TCA 90 GGA TCA GAA GTT CAA AGT TCC TGG GCA GAA ACT ACT TAT TGG ATA TCA 91 Gly Ser Glu Valactin ser Ser Trp Ala Glu Thr Thr Tyr Trp Ile Ser 91 120 125 130 92 125 130	55		(ix) FE	ATUR	€:												
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/815,773

DATE: 04/30/97 TIME: 14:54:35

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102	TAC	AAT	TGG	CAA	TAT	TTA	CTC	TGT	TCT	TGG	AAA	CCT	GGC	ATA	GGT	GTA	537
103	Tyr	Asn	Trp	Gln	Tyr	Leu	Leu	Cys	Ser	Trp	Lys	Pro	Gly	Ile	Gly	Val	
104			150					155					160				
105																	
106	CTT	CTT	GAT	ACC	AAT	TAC	AAC	TTG	TTT	TAC	TGG	TAT	GAG	GGC	TTG	GAT	585
107	Leu		Asp	Thr	Asn	Tyr	Asn	Leu	Phe	Tyr	Trp	Tyr	Glu	Gly	Leu	Asp	
108		165					170					175					
109																	
110						GTT											633
111		Ala	Leu	Gln	Cys	Val	Asp	Tyr	Ile	Lys		Asp	Gly	Gln	Asn		
112	180					185					190					195	
113																	
114						TAT											681
115	GTÀ	Cys	Arg	Phe		Tyr	Leu	Glu	Ala		Asp	Tyr	Lys	Asp		Tyr	
116					200					205					210		
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119	тте	Cys	vaı		GTĀ	Ser	Ser	GLU		Lys	Pro	ITe	Arg		Ser	Tyr	
120				215					220					225			
121	mma			~~~					amm		a a m			~~.	~~~		
122						CAA											777
123 124	Pne	THE		GIN	Leu	Gln	ASN		vaı	гàг	Pro	Leu		Pro	vaı	Tyr	
124			230					235					240				
126	COUR	х стт	mmm	N CITT	aaa	GAG	N CITT	ma x	man	C 3 3	a mm	220	аша	***	maa	3.00	925
125						Glu											825
128	Leu	245	FIIE	1111	Arg	GIU	250	Ser	Cys	GIU	TTE	255	rea	гуѕ	пр	ser	
129		243					250					233					
130	λπа	ССТ	ጥጥር	CCA	ССТ	ATT	CCA	GCA	AGG	ጥርጥ	արարար	αлπ	πλπ	GVV	አ ጥጥ	GAG	873
131						Ile											0/3
132	260	110	пец	Orl	110	265	110	ALU	A. y	Cys	270	изр	- y -	GIU	116	275	
133	200					200					2,0					275	
134																	
135	ATC	AGA	GAA	GAT	GAT	ACT	ACC	TTG	GTG	ACT	GCT	ACA	GTT	GAA	ААТ	GAA	921
136						Thr											, , ,
137		5			280					285					290		
138					-												
139	ACA	TAC	ACC	TTG	AAA	ACA	ACA	AAT	GAA	ACC	CGA	CAA	TTA	TGC	TTT	GTA	969
140	Thr	Tyr	Thr	Leu	Lys	Thr	Thr	Asn	Glu	Thr	Arq	Gln	Leu	Cys	Phe	Val	
141		-		295	•				300		_			305			
142																	
143	GTA	AGA	AGC	AAA	GTG	AAT	ATT	TAT	TGC	TCA	GAT	GAC	GGA	ATT	TGG	AGT	1017
144	Val	Arg	Ser	Lys	Val	Asn	Ile	Tyr	Cys	Ser	Asp	Asp	Gly	Ile	Trp	Ser	
145		_	310	-				315	-		_	-	320		-		
146														•			
147						CAA											1065
148	Glu	Trp	Ser	Asp	Lys	Gln	Cys	Trp	Glu	Gly	Glu	Asp	Leu	Ser	Lys	Lys	
149		325					330					335					
150												•					
151						TGG											1113
152	Thr	Leu	Leu	Arg	Phe	Trp	Leu	Pro	Phe	Gly	Phe	Ile	Leu	Ile	Leu	Val	

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153	340					345					350			Il	N <i>PUT</i>	SET: S1732 355	29.raw
154																	
155																AAA	1161
156	Ile	Phe	Val	Thr		Leu	Leu	Leu	Arg	_	Pro	Asn	Thr	Tyr	Pro	Lys	
157					360					365					370		
158																	
159						TTC				TGA	AGAC'	TTT	CCAT	ATCA.	AG		1208
160	мет	тте	Pro		Pne	Phe	cys	Asp									
161 162				375					380								
163	202	ግ አ መረግ	י גיחים	ጥጥረ! እ ረ	ግሞረግ እ	A (1 A (ammm,	77 X 71	יאט יי	TO CO	~ ~ ~ ~	mem.	דר א אי	nam /	a a ama	CTCAAT	1268
164	AGA	CAIG	GIA	IIGA	JICA	HC A	3111	CCAG	I CA	IGGC	CAAA	161	ICAA	IAT	GAGI	CICAAI	1200
165	λλλι	стса	አ ጥጥ '	TTTC	ኮጥርርር	מ מי											1289
166	6															1207	
167	7																
168	, , , , , , , , , , , , , , , , , , ,																
169						_											
170	(i) SEQUENCE CHARACTERISTICS:																
171	(A) LENGTH: 380 amino acids																
172	(B) TYPE: amino acid																
173	(D) TOPOLOGY: linear																
174	Add Not Equation when a second of the																
175	(ii) MOLECULE TYPE: protein																
176	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:																
177		(:	X1) :	SEQUI	ENCE	DES	CRIP'	rion	: SE	O ID	NO:	2:					
178																	
179 180	Wat	*1-	Dha	17.0.7	a	Т о		T1.	a 1	a	T	m	m1	nh a	T	T1 -	
181	Met 1	Ата	Pile	Vai	Cys 5	Leu	ATG	тте	GIA	Lys 10	Leu	туг	Thr	Pne	Leu 15	TIE	
182	1				3					10					13		
183	Ser	Thr	Thr	Phe	G] v	Cys	Thr	Ser	Ser	Sar	Asn	Фhr	Glu	Tla	L.vg	Val	
184				20		0,5	••••	501	25	DCI	пор		OIU	30	טעם	*41	
185																	
186	Asn	Pro	Pro	Gln	Asp	Phe	Glu	Ile	Val	Asp	Pro	Gly	Tyr	Leu	Gly	Tvr	
187			35		-			40		-		_	45		•	-	
188																	
189	Leu		Leu	Gln	Trp	Gln		Pro	Leu	Ser	Leu	Asp	His	Phe	Lys	Glu	
190		50					55					60					
191	_				_		_	_	_	_	_		- -	_	- -	_•	
192	_	Thr	Val	Glu	Tyr	Glu	Leu	Lys	Tyr	Arg		Ile	Gly	Ser	Glu		
193	65					70					75					80	
194	M	T	m1	-1 -	- 1 -	m\	T	3	.	**!	m	-	•	a1	5 1	•	
195 196	тгр	гÀг	rnr	тте		Thr	гÀг	ASN	Leu		тyr	гàг	Asp	стÀ		Asp	
196					85	•				90					95		
198	T.e.u	Acn	Luc	ردا ت	Tle	Glu	λls	Luc	Tla	uie	Пръ	Len	Leu	Dra	Ψхν	Gln	
199	nea	VO!!	пys	100	116	GIU	TTG	nys	105	1112	IIII	ьeu	neu	110	ттЪ	GTII	
200									± 0 J					110			
201	Cvs	Thr	Asn	Glv	Ser	Glu	Val	Gln	Ser	Ser	Trp	Ala	Glu	Thr	Thr	Tvr	<u> </u>
202	- 1 -		115	1				120					125			- 1	,
203																	:
204	Trp	Ile	Ser	Pro	Gln	Gly	Ile	Pro	Glu	Thr	Lys	Val	Gln	Asp	Met	Asp	
205	-	130				•	135				-	140		-		-	:
																	ţ

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006														IL	IFUI	SEI.
206 207	Cvs	Val	Туг	Tur	Acn	Trn	G] n	Tyr	T. 611	T. 211	Cue	Sor	Trn	Luc	Dro	Gl v
208	145	*41	- 7 -	- y -	ADII	150	0111	ıyı	Беа	пеа	155	261	пр	цуз	FIU	160
209																100
210	Ile	Gly	Val	Leu	Leu	Asp	Thr	Asn	Tyr	Asn	Leu	Phe	Tyr	Trp	Tyr	Glu
211		-			165	-			•	170			- 2 -		175	
212		Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly														
213	Gly	Leu	Asp	His	Ala	Leu	Gln	Cys	Val	Asp	Tyr	Ile	Lys	Ala	Asp	Gly
214	_		_	180				-	185	_	-		-	190	_	_
215																
216	Gln	Asn	Ile	Gly	Cys	Arg	Phe	Pro	Tyr	Leu	Glu	Ala	Ser	Asp	Tyr	Lys
217			195					200					205			
218																
219	Asp		Tyr	Ile	Cys	Val		Gly	Ser	Ser	Glu	Asn	Lys	Pro	Ile	Arg
220		210					215					220				
221			_				_		_		_	_				
222		Ser	Tyr	Phe	Thr		Gln	Leu	Gln	Asn		Val	Lys	Pro	Leu	
223	225					230					235					240
224	D	** - 7	m	.	m1	D I	m1	•	a1	~	~ .	_	~1		_	_
225 226	Pro	vaı	Tyr	Leu	245	Pne	Thr	Arg	GIU		Ser	cys	GIU	тте	_	Leu
225					245					250					255	
228	Luc	Ψrn	Sor	Tla	Dro	LOU	@1 v	Pro	T10	Dro	λla	Λrα	Cvc	Dho	N c n	Птт
229	цуб	115	561	260	110	Dea	OLY	110	265	110	AIG	Arg	Cys	270	изр	ıyı
230				200					203					2,0		
231	Glu	Ile	Glu	Ile	Ara	Glu	Asp	Asp	Thr	Thr	Leu	Val	Thr	Ala	Thr	Val
232			275		5			280					285			
233																
234	Glu	Asn	Glu	Thr	Tyr	Thr	Leu	Lys	Thr	Thr	Asn	Glu	Thr	Arg	Gln	Leu
235		290					295	_				300		_		
236																
237	Cys	Phe	Val	Val	Arg	Ser	Lys	Val	Asn	Ile	Tyr	Cys	Ser	Asp	Asp	Gly
238	305					310					315					320
239		_	_		_	_	_	_		_	_					
240	ITe	Trp	Ser	GLu		Ser	Asp	Lys	Gln	_	Trp	GLu	GTÀ	Glu	_	Leu
241					325					330					335	
242	C	T	T	mh	T	T	1	Dh.	m	.	D	Dh.	a 1	nh -	-1 -	.
243 244	261	гуз	гуз	340	reu	Leu	Arg	Phe	345	Leu	PIO	Pne	сту		тте	Leu
244				340					347					350		
246	Tle	T.e.11	Val	Tle	Phe	Val	Thr	Gly	T. 611	T.011	T.011	λτα	Luc	Dro	Aen	Thr
247		Deu	355	110	1110	vul	****	360	Бец	Бец	nea	nr 9	365	110	ASII	1111
248			000					500					505			
249	Tvr	Pro	Lvs	Met	Ile	Pro	Glu	Phe	Phe	Cvs	Asp	Thr				
250	-] -	370	-1-	,			375			- 1 -	-	380				
251				•												
252						•										
253	(2)	INF	ORMA!	CION	FOR	SEQ	ID 1	10:3	3							
254				à												
255		(i)		_				ESTIC								
256								oase		cs						
257								acid								
258			((2) Si	rani	DEDNI	ESS:	doub	ole							

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